



Db 241 EEGEEOGSDNPFYFDERLSSTRFTEEGHISYLENFYGRSKLLRALKNRYLVLEANPNA 300  
QY 241 EEGEEOGSDNPFYFDERLSSTRFTEEGHISYLENFYGRSKLLRALKNRYLVLEANPNA 300  
Db 301 FYLPHTLDADALLVYIGRGALKMTHDNRRESYNLECGVIRIPAGTFFYLLINRDNNERL 360  
QY 301 FYLPHTLDADALLVYIGRGALKMTHDNRRESYNLECGVIRIPAGTFFYLLINRDNNERL 360  
Db 361 HIAKFLQITSTPGQYKEFFPAGGONPEYLTSTFSEKILEALNTQETKLRGVFGQOREGV 420  
QY 361 HIAKFLQITSTPGQYKEFFPAGGONPEYLTSTFSEKILEALNTQETKLRGVFGQOREGV 420  
Db 421 IIRASQEOIRELTRDSDSRHWHIRRGESSRGPNLFNKRPPLYSNKYGOAYEVKPEDYR 480  
QY 421 IIRASQEOIRELTRDSDSRHWHIRRGESSRGPNLFNKRPPLYSNKYGOAYEVKPEDYR 480  
Db 481 OLQDMDSLVSFIANTVQSGMMGPFFNTRSTKVVVVAASGEADVEMACPHLSGRHGRGGGR 540  
QY 481 OLQDMDSLVSFIANTVQSGMMGPFFNTRSTKVVVVAASGEADVEMACPHLSGRHGRGGGR 540  
Db 541 HEEEDVHYEQVRAKLSKREAIYVLAGHPVYVSSGNENLLFAFGINAQNNHNEFLAGR 600  
QY 541 HEEEDVHYEQVRAKLSKREAIYVLAGHPVYVSSGNENLLFAFGINAQNNHNEFLAGR 600  
Db 601 ERNVLOQIEPQAMELAFAPRKREVEESFNSDQSIFFPGPRHOQOOSPRSTKQOQPLYSI 660  
QY 601 ERNVLOQIEPQAMELAFAPRKREVEESFNSDQSIFFPGPRHOQOOSPRSTKQOQPLYSI 660  
Db 661 LDFVGF 666  
QY 661 LDFVGF 666

RESULT 2  
ID W62829 standard; Protein: 666 AA.  
AC W62829.  
DT 27-OCT-1998 (first entry)  
DE Macadamia integrifolia antimicrobial protein.  
KW antimicrobial protein; infestation; control.  
OS Macadamia integrifolia.  
FS Key Location/Qualifiers  
FT Peptide 1..28  
FT /note= "signal peptide"  
FT Protein 29..666  
FT /note= "mature protein"  
PN W09827805-A1.  
PD 02-JUL-1998.  
PE 22-DEC-1997; AU0874.  
PR 20-DEC-1996; AU-004275.  
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.  
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;  
DR N-PSDB: V42311.  
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -  
PT useful for controlling microbial infestations of plants or mammals  
PS Claim 1; Page 39-41; 96pp; English.  
CC The sequence is that of an antimicrobial protein which can  
CC be used to control microbial infestations in plants and mammalian  
CC animals.  
SQ Sequence 666 AA:

Query Match 96.4%; Score 4746; DB 1; Length 666;  
Best Local Similarity 96.1%; Pred. No. 0.00e+00;  
Matches 640; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

Db 1 MAINSNSCLSLFLSLSTVSLAESEPDROVEECKRCOMLETSGQNRRCVSQCD 60  
QY 1 MAINSNSCLSLFLSLSTVSLAESEPDROVEECKRCOMLETSGQNRRCVSQCD 60  
Db 61 KREEDIDMSKYNDODDPTDCOCORRCROESGPRQOQYQORCKEICEEETYNRQ 120  
QY 61 KREEDIDMSKYNDODDPTDCOCORRCROESGPRQOQYQORCKEICEEETYNRQ 120

Db 121 DPOQYEOGCOERCOHETEPHMTQOQRCERRYEKEKROOKRYEEOQREDEEYEREM 180  
QY 121 DPOQYEOGCOERCOHETEPHMTQOQRCERRYEKEKROOKRYEEOQREDEEYEREM 180  
Db 181 KEEDKRRPOQREYEDCRRRCEDQEPQOQYQORRCRQOQROHGRGGLINPQGGSSRY 240  
QY 181 KEEDKRRPOQREYEDCRRRCEDQEPQOQYQORRCRQOQROHGRGGLINPQGGSSRY 240  
Db 241 EEGEEOGSDNPFYFDERLSSTRFTEEGHISYLENFYGRSKLLRALKNRYLVLEANPNA 300  
QY 241 EEGEEOGSDNPFYFDERLSSTRFTEEGHISYLENFYGRSKLLRALKNRYLVLEANPNA 300  
Db 301 FYLPHTLDADALLVYIGRGALKMTHDNRRESYNLECGVIRIPAGTFFYLLINRDNNERL 360  
QY 301 FYLPHTLDADALLVYIGRGALKMTHDNRRESYNLECGVIRIPAGTFFYLLINRDNNERL 360  
Db 361 HIAKFLQITSTPGQYKEFFPAGGONPEYLTSTFSEKILEALNTQETKLRGVFGQOREGV 420  
QY 361 HIAKFLQITSTPGQYKEFFPAGGONPEYLTSTFSEKILEALNTQETKLRGVFGQOREGV 420  
Db 421 IIRASQEOIRELTRDSDSRHWHIRRGESSRGPNLFNKRPPLYSNKYGOAYEVKPEDYR 480  
QY 421 IIRASQEOIRELTRDSDSRHWHIRRGESSRGPNLFNKRPPLYSNKYGOAYEVKPEDYR 480  
Db 481 OLQDMDSLVSFIANTVQSGMMGPFFNTRSTKVVVVAASGEADVEMACPHLSGRHGRGGGR 540  
QY 481 OLQDMDSLVSFIANTVQSGMMGPFFNTRSTKVVVVAASGEADVEMACPHLSGRHGRGGGR 540  
Db 541 HEEEDVHYEQVRAKLSKREAIYVLAGHPVYVSSGNENLLFAFGINAQNNHNEFLAGR 600  
QY 541 HEEEDVHYEQVRAKLSKREAIYVLAGHPVYVSSGNENLLFAFGINAQNNHNEFLAGR 600  
Db 601 ERNVLOQIEPQAMELAFAPRKREVEESFNSDQSIFFPGPRHOQOOSPRSTKQOQPLYSI 660  
QY 601 ERNVLOQIEPQAMELAFAPRKREVEESFNSDQSIFFPGPRHOQOOSPRSTKQOQPLYSI 660  
Db 661 LDFVGF 666  
QY 661 LDFVGF 666

RESULT 3  
ID W62830 standard; Protein: 625 AA.  
AC W62830.  
DT 27-OCT-1998 (first entry)  
DE Macadamia integrifolia antimicrobial protein.  
KW antimicrobial protein; infestation; control.  
OS Macadamia integrifolia.  
FS Key Location/Qualifiers  
FT Peptide 1..28  
FT /note= "signal peptide"  
FT Protein 29..666  
FT /note= "mature protein"  
PN W09827805-A1.  
PD 02-JUL-1998.  
PE 22-DEC-1997; AU0874.  
PR 20-DEC-1996; AU-004275.  
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.  
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;  
DR N-PSDB: V42311.  
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -  
PT useful for controlling microbial infestations of plants or mammals  
PS Claim 1; Page 43-45; 96pp; English.  
CC The sequence is that of an antimicrobial protein which can  
CC be used to control microbial infestations in plants and mammalian  
CC animals.  
SQ Sequence 625 AA:

Query Match 91.1%; Score 4487; DB 1; Length 625;  
Best Local Similarity 96.6%; Pred. No. 0.00e+00;  
Matches 604; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

D	b	1	QCMQLETSQGMARCSQCDKRFEEIDMSKTDNDQEDPTEQCCQRCRCRQDESPRRQY	60
Q	y	42	QCMQLETSQGMARCSQCDKRFEEIDMSKTDNDQEDPTEQCCQRCRCRQDESPRRQY	101
D	b	61	CORCKEICEEETEEENRRDPQOQYEQCCQRCRCRQDESPRRQY	120
Q	y	102	CORCKEICEEETEEENRRDPQOQYEQCCQRCRCRQDESPRRQY	161
D	b	121	QKRYEQQREDEEKEEYERKKEGDKRDPQREYEDCRRHCQDEPRLOYCCQRCQDEQR	180
Q	y	162	QKRYEQQREDEEKEEYERKKEGDKRDPQREYEDCRRHCQDEPRLOYCCQRCQDEQR	221
D	b	181	QHRGRCGLMNRQGGSGRYEEGEKEQSNPRYPEDRSISTFRREBHSIYLENFYRSK	240
Q	y	222	QHRGRCGLMNRQGGSGRYEEGEKEQSNPRYPEDRSISTFRREBHSIYLENFYRSK	281
D	b	241	LIRALKNRYLVLEENPAPAFVPHLDADALLYIGGRGALKMHRNRESYNLEGGDVI	300
Q	y	282	LIRALKNRYLVLEENPAPAFVPHLDADALLYIGGRGALKMHRNRESYNLEGGDVI	341
D	b	301	RIPAGTFYVLINRDNNERLHIAKFLQTIISTPGQYKEFFPAGQNPDEYLSFTFSKEILEA	360
Q	y	342	RIPAGTFYVLINRDNNERLHIAKFLQTIISTPGQYKEFFPAGQNPDEYLSFTFSKEILEA	401
D	b	361	LNTQTERIRGVLGQOREVITIRASQEQRLRTTRDSSRRKHTIRGESSRGPNYLNFKR	420
Q	y	402	LNTQTERIRGVLGQOREVITIRASQEQRLRTTRDSSRRKHTIRGESSRGPNYLNFKR	461
D	b	421	PLYSNKYQAAVEVPEDYRQLODMDSVFYINATIQGSMGCFEFTSTRSTKYVVAASGADV	480
Q	y	462	PLYSNKYQAAVEVPEDYRQLODMDSVFYINATIQGSMGCFEFTSTRSTKYVVAASGADV	521
D	b	481	EMACPHTLSGRHGGGGRKHEEVEVHYEYVRAFLSKREALIVLAGHPVVFVSGNENL	540
Q	y	522	EMACPHTLSGRHGGGGRKHEEVEVHYEYVRAFLSKREALIVLAGHPVVFVSGNENL	581
D	b	541	LFAGGINQNNHNFVLAGRENNVLOQIEPOMMELAFAPASREVEELFNSODESTFFPGPR	600
Q	y	582	LFAGGINQNNHNFVLAGRENNVLOQIEPOMMELAFAPASREVEELFNSODESTFFPGPR	641
D	b	601	QHQQQSPRSTKQOQPLVSIIDFVGF 625	
Q	y	642	QHQQQSPRSTKQOQPLVSIIDFVGF 666	
RESULT 4				
ID	R20181 standard; Protein; 566 AA.			
AC	R20181;			
DT	16-APR-1992 (first entry)			
DE	Sequence encoded by 67 kd T. cacao protein cDNA.			
KW	Cocoa: flavour; vicillin; seed storage protein.			
OS	Theobroma cacao.			
PN	W09119801.A.			
PD	26-DEC-1991.			
PF	07-JUN-1991: G00914.			
PR	11-JUN-1990: GB-013016.			
PA	(MRSCL) MARS UK LTD.			
PI	Spencer ME, Hodge R, Deakin EA, Ashton S;			
DR	WPI: 92-02418/03.			
DR	N-PSDB: 020377.			
PT	Recombinant cocoa proteins - are responsible for flavour in cocoa beans and produced in large quantities using yeast and bacterial expression vectors			
PS	Claim 4; Fig 2; 59pp; English.			
CC	The inventors claim a 67 kD and 31 kD T. cacao protein, and fragments, and encoding DNAs. The 47 kD and 31 kD proteins are derived from the 67 kD precursor. T. cacao protein cDNA was detected in a cDNA library prepared from immature cocoa beans RNA using a probe based on the AA sequence of a CNBR peptide common to the 47 kD and 31 kD polypeptides. Homology searches revealed close			
CC	homologies between the 67 kD polypeptide and the vicillins, which are seed storage proteins.			

Sequence 566 AA; Query Match 27.0%; Score 1330; DB 1; Length 566;  
Best Local Similarity 39.7%; Pred. No. 4,66e-106;  
Matches 215; Conservative 146; Mismatches 153; Indels 27; Gaps 21.

Dd ERDPQOYECORCESE-AEEDEE-QCE--ORCRE-YKEGOQROEE-E-LQHQY 86  
|::: :||:| | | | | | | | | | | | | | | | | | | | | |  
Qy ETEPHM-OIQQRERREYEKKRQKRYEDQREDEEYEEMKKEKDNDPOOREYE 195  
87 OCGGCOEOGOGOREDOOCCKWCEQKEDEGEENYHNH-KNRSEEGOGRNPY 145  
Qy DCRRC-EGOE-PQOHOCQLRCEQORQHGGDDMNPPRGSGRRLEDEEESDNPY 253  
146 FPKRSFOTREFDEGNFKILQFAENSPLKINDYRLAMEANPTFILPHHCAEI 205  
Qy FDER-SLSTRTEEGLTSYLENFGSKLLRALKNRYLVLEANPVAFLPTHDAI 312  
254 FDER-SLSTRTEEGLTSYLENFGSKLLRALKNRYLVLEANPVAFLPTHDAI 312  
Db YFYNGKGTITFYVHENKESINVRGVSVSPAGSTYYVSODNQELTAVIALPVNSP 265  
Qy LLYVGREALMIHHDRNESYNLCGGVIRIPACTTYILLRNNEHLTAFLQTISTP 372  
313 LLYVGREALMIHHDRNESYNLCGGVIRIPACTTYILLRNNEHLTAFLQTISTP 372  
Db KYELFPAGNKRESYGATSYVLTFVTQREKLTELLEBORGKRQOGQGMFRKA 325  
Qy 373 GOYKEFPAGQNEPILTSTSKILEALNTQEKRGVFGQOREGITRASQEQREL 432  
373 GOYKEFPAGQNEPILTSTSKILEALNTQEKRGVFGQOREGITRASQEQREL 432  
Db KPEDIRAISQATSPRHGERLAINELSOPYSNONGFEFFACPEDFSOFONMDVAVS 385  
Qy 433 TRDD--SSSRMHRIHRGESSRGYNLFNRPPLSNKYGAIVEKPEDYQOLDMLSVF 450  
Db AFKLNGAIEVPHYNSKATVEVTDGYAQAACPILSKSQOSQSGRODRREQEISE 445  
Qy 491 IANTOGSMGPFTNFTRSTKVYVVASGEADVEMACPLSGR-HGGRGC-GKR-HEEE-- 544  
Db EEETGEFOVAPLSPGDVFAPAARGVHTFEASDQCLNVAAFGNLANNONRIFLGK-R 504  
Qy 545 EDV--HYEQVARISKREAIYVLGHVYVVSSGENELLFLPAFGINQNHNHPLAGRER 602  
Db NLYVRQMSAEAKLEFGVPKSLVDNIENNPDSE-YFMFSQ-QHOR-RDERGNPLASIID 561  
Qy 603 NVLDQIFQAMELAFAPRKVESESFNSQSISFIFFPRRHQQDSPRSTKQOPLYSIID 662

Dd 562 F 562.  
|  
Qy 663 F 663

RESULT 5  
ID W62832 standard; Protein; 590 AA.  
AC W62832;  
DT 27-OCT-1998 (first entry)  
DE Gossypium hirsutum antimicrobial protein.  
KW antimicrobial protein; infestation; control.  
KS Gossypium hirsutum.  
PN WO9827805-A1.  
PD 02-JUL-1998.  
PF 22-DEC-1997; AU0874.  
PR 20-DEC-1996; AU-004275.  
RA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.  
PI Bower NI, Goulier KA, Green JL, Manners JW, Marcus JP;  
DR WPJ; 98-377219/32.  
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -  
PS useful for controlling microbial infestations of plants or mammals  
CC Claim 1, Page 49-51; 96pp; English.  
The sequence is that of an antimicrobial protein which can  
be used to control microbial infestations in plants and mammalian  
animals.  
SQ Sequence 590 AA;

Query Match 25.3%; Score 1246; DB 1; Length 590;  
Best Local Similarity 39.3%; Pred. No. 2.04e-98;  
Matches 223; Conservative 150; Mismatches 144; Indels 47; Gaps 29;





OY 367 Q-TISTPGQYKEFPFAGGONPEPYLSTFSKELLEALNTOTKEKLGVCQOEGVITIRAS 425  
DB 287 REOVVALAPTAKSSW-WPF--GGEES-KPOFINFSKRPTISNGYRLTEVGPPDDDEKSMQ 342  
OY 426 QOQIELTRDSESRHWHIRRGESSRGYPNLFNKRPLXSNKYGAUYEKPEDY-RQ-LQ 483  
DB 343 RLNLMLFTNTITORSNSTIHYNSHATKIALVIDRGHLOISCPHMSR--SSHS--K-HDK 398  
OY 484 DMDLSVFIANVTOGSMGPFEPFTRSTKYVVVAVSGEADVEMACPHLSGRHGGGGRHDE 543  
DB 399 SSPS-YHRISDLKPGMVFVPPGHPFTIASNKENLMIICEFVARDKK-KFTFAGKD- 455  
OY 544 EEDVHYEQVRAKLSKREALIVLAGHPVYVSSGNENLLFAFGINAKNHNENF-LAGRRER 602  
DB 456 NIVSSLDNVAKELEAFNYPSEMNGVF 481  
OY 603 NVLQGLEPQAMELAFAPRKEVEESF 628  
RESULT 10  
ID W90340 standard; protein: 444 AA.  
AC W90340;  
DT 24-MAY-1999 (first entry)  
DE G. max truncated SBP1 protein.  
KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;  
KM seed; carbohydrate content; soybean.  
OS Glycine max.  
PN W09853086-A1.  
PD 26-NOV-1998.  
PF 21-MAY-1998: U10465.  
PR 22-MAY-1997: US-047568.  
PI (UNIT) UNIV WASHINGTON STATE RES FOUND.  
PI Chao WS, Gimes HD;  
DR WPI, 99-070155/06.  
PT New modified plant sucrose binding proteins - used to develop  
transgenic plants which can have enhanced or decreased sucrose  
uptake activity in developing seeds  
PT Claim 7; Page 36-37; 58pp; English.  
CC This sequence represents a novel sucrose binding protein, SBP1 isolated  
from glycine max. This protein is used in a method resulting in the  
production of a modified plant sucrose binding protein (SBP) which has a  
modified amino acid sequence compared to a corresponding wild-type SBP,  
and where expression of the modified SBP in a yeast assay system confers  
enhanced sucrose uptake compared to the corresponding wild-type SBP.  
CC The products of the invention can be used for producing transgenic plants  
which have modified sucrose uptake activity, particularly in developing  
seeds. Enhanced sucrose uptake activity in developing seeds may be  
desirable where it is an advantage to increase the carbohydrate content,  
such as soybean). In contrast, decreased sucrose uptake activity in  
seeds might be desirable where the vegetative material of the plant is  
harvested. The SBP regulatory regions confer specific or enhanced  
expression in developing seeds and so may be used to express any  
transgene in developing seeds.  
CC Sequence 444 AA.

Query Match 19.6%; Score 964; DB 1; Length 444;  
Best Local Similarity 38.8%; Pred.No. 6.98e-73;  
Matches 158; Conservative 109; Mismatches 123; Indels 17; Gaps 15;

DB 49 QOQYTEGDKRYCLOCDRIYHMKQREKQIO-EETRF-KKEEESREDEEOEOHEOD 106  
OY 190 QOREY-EDCRRCEDOEPRQOQOCLRCREOOROGRGDMNPNRGSGRGEES 248  
DB 107 EBPYFEEDKDEFTVETGGRIRYLKFKTEKSKLLOGTENRLAILERATFVSPPRF 166  
OY 249 DNPYTFDE-RSSTRREEGHISVENYGRSKLRALKNRLLVLEENPAFVLPPLTL 307  
DB 167 DSEVFFFNKRAVLGIVSESETEKITLPEGDMIHIPAGTPYIYVNRDENLFLAMLHI 226  
OY 308 DADAILVIGSGALKMHIHNDRESYNLECGDVIIRPATFTYLLINRDNNELHLIAKF-L 366  
DB 227 PYSVSTPGKEFEFFAPGGRDPSVLSASWNVLAALQTPKGLLENVDOQNEGSIFRIS 286

OY 367 Q-TISTPGQYKEFPFAGGONPEPYLSTFSKELLEALNTOTKEKLGVCQOEGVITIRAS 425  
DB 287 REOVVALAPTAKSSW-WPF--GGEES-KPOFINFSKRPTISNGYRLTEVGPPDDDEKSMQ 342  
OY 426 QOQIELTRDSESRHWHIRRGESSRGYPNLFNKRPLXSNKYGAUYEKPEDY-RQ-LQ 483  
DB 343 RLNLMLFTNTITORSNSTIHYNSHATKIALVIDRGHLOISCPHMSR--SSHS--K-HDK 398  
OY 484 DMDLSVFIANVTOGSMGPFEPFTRSTKYVVVAVSGEADVEMACPHLSGRHGGGGRHDE 543  
DB 399 SSPS-YHRISDLKPGMVFVPPGHPFTIASNKENLMIICEFVAR 444  
OY 544 EEDVHYEQVRAKLSKREALIVLAGHPVYVSSGNENLLFAFGINAO 590  
RESULT 11  
ID W62838 standard; protein: 605 AA.  
AC W62838;  
DT 27-OCT-1998 (first entry)  
DE Glycine max antimicrobial protein.  
KW antimicrobial protein; infestation; control.  
OS Glycine max.  
PN W09827805-A1.  
PD 02-JUL-1998.  
PF 22-DEC-1997: A00874.  
PR 20-DEC-1996: AU-004275.  
PI (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.  
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;  
DR WPI, 98-372729/32.  
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -  
useful for controlling microbial infestations of plants or mammals  
PT Claim 1; Page 63-65; 96pp; English.  
CC The sequence is that of an antimicrobial protein which can  
be used to control microbial infestations in plants and mammalian  
CC animals.  
CC Sequence 605 AA;

Query Match 18.9%; Score 930; DB 1; Length 605;  
Best Local Similarity 32.7%; Pred.No. 8.08e-70;  
Matches 193; Conservative 160; Mismatches 197; Indels 41; Gaps 32;

DB 38 CLOCSNERSDYRNA-CHARCNLKYKECESEETPRPR-PRQ-HPEREPOQGEKE 94  
OY 85 CORCROQESGRQOQYQORCKELCEEEENRQROPOQOYEOCQORRETERPMQ 144  
DB 95 EDEDE-OPR-PIPFPRPOP-OOEEHEOREE-OEWPRKEE-KRGEKSEED-EDEDEQ 148  
OY 145 TCQOCERRYEKERKKQOKRIEBOQREDEKYEERMKEDNKRPOQREYEDCRRCQO 204  
DB 149 DERQPPFRPHQKEERNEEDEDE-EOQRESEES-EDSELRRHKNKPNFLFGSNRFTL 206  
OY 205 EPRQHQOQLCREQOQRHGRGDMNPNRGSGRYEGE-EDQSD-NPYFDEMSLSTR 262  
DB 207 FKNQYGRIRVLORENORSPOLONLDRYILEFNKSPNTLLPNHADYLLVINGTAIL 266  
OY 263 FTEGHGTSVLENFEGRSKLRALKNYRLVLEENPAFVLPPTHIDADAILVIGRGAL 322  
DB 267 SLVNNDDSDSYRLQSGDRLVPSGTYVYVNPDDNENRLTLLIAPVKKPGRFSFELS 325  
OY 323 KNIHNDNESTNLECGDVIIRIPAGTFTYLLINRDNNERHLIAKFIQTIOTISTPGQYKEFPFAG 382  
DB 327 TEAOQSYQGSRNILASVDTKEEINKVLFSEEGQOQOERLOESVYIEISKEQIRA 386  
OY 383 GONPEPYLSTFSKELLEALNTQ--TE--K-L-R-GVF-GQOR--EGVIRASQOQIRE 431  
DB 387 LSKRAKSSRK-TI--SEED-K-PENLRSDPIYSNKIKGFEFTPEKNPOLRDLDFLS 441  
OY 422 LT-RDSDSRRHWHIRRGESSRGYPNLFNKRPLXSNKYGAUYEKPEDYROLQMDLSVF 490  
DB 442 IVDNMEGALLPHFNSKALIVLVINEGDANIELV-G-LKEQO--OE--QOQOEPLEVR 494  
OY 491 IANVTOGSMGPFEPFTRSTKYVVVAVSGEADVEMACPHLSGRHGGGGRHDEEDVHYE 550







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QY 296 ANPNAPVLPHTLDDALLVYIGRGALKMIHNDRESYNLECGDVIRIPACTTYLINRD 355
Db 273 DNQNLRAKISMYPVNTPGQFEDFPASSRDQSSYLQGSRNLTLEAFNAEFNEIRVYLE 332
QY 356 NNERLHIAKFIQTISTPGQYKEFPAGQNPBYLSTFSKEITLALNTQTEKLRGYE-- 413
Db 333 ENAGGEQEEERGQRRSTRSSDNQYIVKSKENHVOELTKHAKSVSKGSEEDITNPINL 392
QY 414 ---GQGRE-GVI---IRASQEQ--IRELTRDQS-E-SRH-WHI-RGGE-S-RGPNL 457
Db 393 RDGEPRDLSNNPGRLEFVYKPPDKKNPOLDDMLTCEIKGALMLPHNSKAWIYVYVK 452
QY 458 FNKRPLYSNKTIGQAYEVKPED-YRQLOMDLSYFIANVTQSGMGPFFNTSTKVAVVAS 516
Db 453 GTGNLELVAVRKQEQQGRGREQEWEEDEEEDSNNREYRYTARLKEGDFVIMPAAHP 512
QY 517 GEADVEMACPHLSGRHGRGGKRRHEEDVHYE---QVR---ARLSKREAIYVLAGHP 569
Db 513 VA-YNASSE-LHLIGGINAENNRIFLAGDKDNVTDQIEKQAKDLAFPGSGEOVEKLIK 570
QY 570 VVEVSSGNENLLLEAFGINQNNHENFLAGRERNVLOQIEQAMELAFAPRKEVEESFN 629
Db 571 NQRES-HFVSARPOSQSPSPKEDQ 595
QY 630 SQDOSITFFPGPROHOQOSPRSTKQOQ 655

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Search completed: Sat May 13 08:01:29 2000  
 Job time : 28 secs.

